



20093A-21US-Substitute Sequence Listing.txt
SEQUENCE LISTING

<110> Murphy, Gerald P.
Boynton, Alton L.
Sehgal, Anil

<120> Nr-CAM GENE, NUCLEIC ACIDS AND NUCLEIC ACID PRODUCTS
FOR THERAPEUTIC AND DIAGNOSTIC USES FOR TUMORS

<130> 20093A-002100US

<140> 09/301,380

<141> 1999-04-27

<150> 60/112,098

<151> 1998-12-14

<150> 60/083,152

<151> 1998-04-27

<160> 33

<170> PatentIn Ver. 2.0

<210> 1

<211> 4134

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (130)..(4029)

<400> 1

cttcaaagtt ccccgcatga aaattactta aacgttgcac acaacgtttc agaaaatctt 60

ttgtgaaaga agaaaaggaa attcagtgtg tgagtctcag caggagttaa gctaatagcag 120

cttaaaata atg ccg aaa aag aag cgc tta tct gcg ggc aga gtg ccc ctg 171
Met Pro Lys Lys Lys Arg Leu Ser Ala Gly Arg Val Pro Leu
1 5 10

att ctc ttc ctg tgc cag atg att agt gca ctg gaa gta cct ctt gat 219
Ile Leu Phe Leu Cys Gln Met Ile Ser Ala Leu Glu Val Pro Leu Asp
15 20 25 30

cca aaa ctt ctt gaa gac ttg gta cag cct cca acc atc acc caa cag 267
Pro Lys Leu Leu Glu Asp Leu Val Gln Pro Pro Thr Ile Thr Gln Gln
35 40 45

tct cca aaa gat tac att att gac cct cgg gag aat att gta atc cag 315
Ser Pro Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile Val Ile Gln
50 55 60

tgt gaa gcc aaa ggg aaa ccg ccc cca agc ttt tcc tgg acc cgt aat 363
Cys Glu Ala Lys Gly Lys Pro Pro Pro Ser Phe Ser Trp Thr Arg Asn
65 70 75

ggg act cat ttt gac atc gat aaa gac cct ctg gtc acc atg aag cct 411
Gly Thr His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr Met Lys Pro
80 85 90

ggc aca gga acg ctc ata att aac atc atg agc gaa ggg aaa gct gag 459
Gly Thr Gly Thr Leu Ile Ile Asn Ile Met Ser Glu Gly Lys Ala Glu
95 100 105 110

acc tat gaa gga gtc tat cag tgt aca gca agg aac gaa cgc gga gct 507

20093A-21US-Substitute Sequence Listing.txt

Thr	Tyr	Glu	Gly	Val	Tyr	Gln	Cys	Thr	Ala	Arg	Asn	Glu	Arg	Gly	Ala	
115									120					125		
gca	ggt	tct	aat	aac	att	ggt	gtc	cgc	cca	tcc	aga	tca	cca	ttg	tgg	555
Ala	Val	Ser	Asn	Asn	Ile	Val	Val	Arg	Pro	Ser	Arg	Ser	Pro	Leu	Trp	
			130					135					140			
acc	aaa	gaa	aaa	ctt	gaa	cca	atc	aca	ctt	caa	agt	ggt	cag	tct	tta	603
Thr	Lys	Glu	Lys	Leu	Glu	Pro	Ile	Thr	Leu	Gln	Ser	Gly	Gln	Ser	Leu	
		145					150					155				
gta	ctt	ccc	tgc	aga	ccc	cca	att	gga	tta	cca	cca	cct	ata	ata	ttt	651
Val	Leu	Pro	Cys	Arg	Pro	Pro	Ile	Gly	Leu	Pro	Pro	Pro	Ile	Ile	Phe	
	160					165					170					
tgg	atg	gat	aat	tcc	ttt	caa	aga	ctt	cca	caa	agt	gag	aga	ggt	tct	699
Trp	Met	Asp	Asn	Ser	Phe	Gln	Arg	Leu	Pro	Gln	Ser	Glu	Arg	Val	Ser	
175				180						185				190		
caa	ggt	ttg	aat	ggg	gac	ctt	tat	ttt	tcc	aat	gtc	ctc	cca	gag	gac	747
Gln	Gly	Leu	Asn	Gly	Asp	Leu	Tyr	Phe	Ser	Asn	Val	Leu	Pro	Glu	Asp	
				195					200					205		
acc	cgc	gaa	gac	tat	atc	tgt	tat	gct	aga	ttt	aat	cat	act	caa	acc	795
Thr	Arg	Glu	Asp	Tyr	Ile	Cys	Tyr	Ala	Arg	Phe	Asn	His	Thr	Gln	Thr	
			210					215					220			
ata	cag	cag	aag	caa	cct	att	tct	gtg	aag	gtg	att	tca	gtg	gat	gaa	843
Ile	Gln	Gln	Lys	Gln	Pro	Ile	Ser	Val	Lys	Val	Ile	Ser	Val	Asp	Glu	
		225					230					235				
ttg	aat	gac	act	ata	gct	gct	aat	ttg	agt	gac	act	gag	ttt	tat	ggt	891
Leu	Asn	Asp	Thr	Ile	Ala	Ala	Asn	Leu	Ser	Asp	Thr	Glu	Phe	Tyr	Gly	
	240					245					250					
gct	aaa	tca	agt	aga	gag	agg	cca	cca	aca	ttt	tta	act	cca	gaa	ggc	939
Ala	Lys	Ser	Ser	Arg	Glu	Arg	Pro	Pro	Thr	Phe	Leu	Thr	Pro	Glu	Gly	
255					260					265				270		
aat	gca	agt	aac	aaa	gag	gaa	tta	aga	gga	aat	gtg	ctt	tca	ctg	gag	987
Asn	Ala	Ser	Asn	Lys	Glu	Glu	Leu	Arg	Gly	Asn	Val	Leu	Ser	Leu	Glu	
				275					280					285		
tgc	att	gca	gaa	gga	ctg	cct	acc	cca	att	att	tac	tgg	gca	aag	gaa	1035
Cys	Ile	Ala	Glu	Gly	Leu	Pro	Thr	Pro	Ile	Ile	Tyr	Trp	Ala	Lys	Glu	
			290					295					300			
gat	gga	atg	cta	ccc	aaa	aac	agg	aca	ggt	tat	aag	aac	ttt	gag	aaa	1083
Asp	Gly	Met	Leu	Pro	Lys	Asn	Arg	Thr	Val	Tyr	Lys	Asn	Phe	Glu	Lys	
		305					310					315				
acc	ttg	cag	atc	att	cat	ggt	tca	gaa	gca	gac	tct	gga	aat	tac	caa	1131
Thr	Leu	Gln	Ile	Ile	His	Val	Ser	Glu	Ala	Asp	Ser	Gly	Asn	Tyr	Gln	
	320					325					330					
tgt	ata	gca	aaa	aat	gca	tta	gga	gcc	atc	cac	cat	acc	att	tct	gtt	1179
Cys	Ile	Ala	Lys	Asn	Ala	Leu	Gly	Ala	Ile	His	His	Thr	Ile	Ser	Val	
335					340					345				350		
aga	ggt	aaa	gca	gct	cca	tac	tgg	atc	aca	gcc	cct	caa	aat	ctt	gtg	1227
Arg	Val	Lys	Ala	Ala	Pro	Tyr	Trp	Ile	Thr	Ala	Pro	Gln	Asn	Leu	Val	
				355					360					365		
ctg	tcc	cca	gga	gag	gat	ggg	acc	ttg	atc	tgc	aga	gct	aat	ggc	aac	1275
Leu	Ser	Pro	Gly	Glu	Asp	Gly	Thr	Leu	Ile	Cys	Arg	Ala	Asn	Gly	Asn	
			370					375					380			

20093A-21US-Substitute Sequence Listing.txt

ccc	aaa	ccc	aga	att	agc	tgg	tta	aca	aat	gga	gtc	cca	ata	gaa	att	1323
Pro	Lys	Pro	Arg	Ile	Ser	Trp	Leu	Thr	Asn	Gly	Val	Pro	Ile	Glu	Ile	
		385					390					395				
gcc	cct	gat	gac	ccc	agc	aga	aaa	ata	gat	ggc	gat	acc	att	att	ttt	1371
Ala	Pro	Asp	Asp	Pro	Ser	Arg	Lys	Ile	Asp	Gly	Asp	Thr	Ile	Ile	Phe	
	400					405					410					
tca	aat	gtt	caa	gaa	aga	tca	agt	gca	gta	tat	cag	tgc	aat	gcc	tct	1419
Ser	Asn	Val	Gln	Glu	Arg	Ser	Ser	Ala	Val	Tyr	Gln	Cys	Asn	Ala	Ser	
					420					425					430	
aat	gaa	tat	gga	tat	tta	ctg	gca	aac	gca	ttt	gta	aat	gtg	ctg	gct	1467
Asn	Glu	Tyr	Gly	Tyr	Leu	Leu	Ala	Asn	Ala	Phe	Val	Asn	Val	Leu	Ala	
				435					440					445		
gag	cca	cca	cga	atc	ctc	aca	cct	gca	aac	aca	ctc	tac	cag	gtc	att	1515
Glu	Pro	Pro	Arg	Ile	Leu	Thr	Pro	Ala	Asn	Thr	Leu	Tyr	Gln	Val	Ile	
			450					455					460			
gca	aac	agg	cct	gct	tta	cta	gac	tgt	gcc	ttc	ttt	ggg	tct	cct	ctc	1563
Ala	Asn	Arg	Pro	Ala	Leu	Leu	Asp	Cys	Ala	Phe	Phe	Gly	Ser	Pro	Leu	
		465					470					475				
cca	acc	atc	gag	tgg	ttt	aaa	gga	gct	aaa	gga	agt	gct	ctt	cat	gaa	1611
Pro	Thr	Ile	Glu	Trp	Phe	Lys	Gly	Ala	Lys	Gly	Ser	Ala	Leu	His	Glu	
						485					490					
gat	att	tat	gtt	tta	cat	gaa	aat	gga	act	ttg	gaa	atc	aaa	gat	gct	1659
Asp	Ile	Tyr	Val	Leu	His	Glu	Asn	Gly	Thr	Leu	Glu	Ile	Lys	Asp	Ala	
					500					505					510	
aca	tgg	atc	gtt	aaa	gaa	att	cct	gtg	gcc	caa	aag	gac	agt	aca	gga	1707
Thr	Trp	Ile	Val	Lys	Glu	Ile	Pro	Val	Ala	Gln	Lys	Asp	Ser	Thr	Gly	
				515					520					525		
act	tat	acg	tgt	gtt	gca	agg	aat	aaa	tta	ggg	atg	gca	aag	aat	gaa	1755
Thr	Tyr	Thr	Cys	Val	Ala	Arg	Asn	Lys	Leu	Gly	Met	Ala	Lys	Asn	Glu	
			530					535					540			
gtt	cac	tta	cag	ccc	gaa	tat	gca	gtt	gtg	caa	aga	ggg	agc	atg	gtg	1803
Val	His	Leu	Gln	Pro	Glu	Tyr	Ala	Val	Val	Gln	Arg	Gly	Ser	Met	Val	
		545					550					555				
tcc	ttt	gaa	tgc	aaa	gtg	aaa	cat	gat	cac	acc	tta	tcc	ctc	act	gtc	1851
Ser	Phe	Glu	Cys	Lys	Val	Lys	His	Asp	His	Thr	Leu	Ser	Leu	Thr	Val	
	560					565					570					
ctg	tgg	ctg	aag	gac	aac	agg	gaa	ctg	ccc	agt	gat	gaa	agg	ttc	act	1899
Leu	Trp	Leu	Lys	Asp	Asn	Arg	Glu	Leu	Pro	Ser	Asp	Glu	Arg	Phe	Thr	
					580					585					590	
gtt	gac	aag	gat	cat	cta	gtg	gta	gct	gat	gtc	agt	gac	gat	gac	agc	1947
Val	Asp	Lys	Asp	His	Leu	Val	Val	Ala	Asp	Val	Ser	Asp	Asp	Asp	Ser	
				595					600					605		
ggg	acc	tac	acg	tgt	gtg	gcc	aac	acc	act	ctg	gac	agc	gtc	tcc	gcc	1995
Gly	Thr	Tyr	Thr	Cys	Val	Ala	Asn	Thr	Thr	Leu	Asp	Ser	Val	Ser	Ala	
			610					615					620			
agc	gct	gtg	ctt	agc	gtt	gtt	gct	cct	act	cca	act	cca	gct	ccc	gtt	2043
Ser	Ala	Val	Leu	Ser	Val	Val	Ala	Pro	Thr	Pro	Thr	Pro	Ala	Pro	Val	
		625					630					635				
tac	gat	gtc	cca	aat	cct	ccc	ttt	gac	tta	gaa	ctg	aca	gat	caa	ctt	2091
Tyr	Asp	Val	Pro	Asn	Pro	Pro	Phe	Asp	Leu	Glu	Leu	Thr	Asp	Gln	Leu	
	640					645					650					

20093A-21US-Substitute Sequence Listing.txt

gac Asp 655	aaa Lys	agt Ser	gtt Val	cag Gln 660	ctg Leu 660	tca Ser	tgg Trp	acc Thr	cca Pro	ggc Gly 665	gat Asp	gac Asp	aac Asn	aat Asn	agc Ser 670	2139
ccc Pro	att Ile	aca Thr	aaa Lys	ttc Phe 675	atc Ile	atc Ile	gaa Glu	tat Tyr	gaa Glu 680	gat Asp	gca Ala	atg Met	cac His	aag Lys 685	cca Pro	2187
ggg Gly	ctg Leu	tgg Trp	cac His 690	cac His	caa Gln	act Thr	gaa Glu	gtt Val 695	tct Ser	gga Gly	aca Thr	cag Gln 700	acc Thr	aca Thr	gcc Ala	2235
cag Gln	ctg Leu	aag Lys 705	ctg Leu	tct Ser	cct Pro	tac Tyr	gtg Val 710	aac Asn	tac Tyr	tcc Ser	ttc Phe	cgc Arg 715	gtg Val	atg Met	gca Ala	2283
gtg Val 720	aac Asn	agc Ser	att Ile	ggg Gly	aag Lys	agc Ser 725	ttg Leu	ccc Pro	agc Ser	gag Glu	gcg Ala 730	tct Ser	gag Glu	cag Gln	tat Tyr	2331
ttg Leu 735	acg Thr	aaa Lys	gcc Ala	tca Ser	gaa Glu 740	cca Pro	gat Asp	aaa Lys	aac Asn	ccc Pro 745	aca Thr	gct Ala	gtg Val	gaa Glu	gga Gly 750	2379
ctg Leu	gga Gly	tca Ser	gag Glu	cct Pro 755	gat Asp	aat Asn	ttg Leu	gag Glu	att Ile 760	acg Thr	tgg Trp	aag Lys	ccc Pro	ttg Leu 765	aat Asn	2427
ggt Gly	ttc Phe	gaa Glu	tct Ser 770	aat Asn	ggg Gly	cca Pro	ggc Gly	ctt Leu 775	cag Gln	tac Tyr	aaa Lys	gtt Val	agc Ser 780	tgg Trp	cgc Arg	2475
cag Gln	aaa Lys	gat Asp 785	ggt Gly	gat Asp	gat Asp	gaa Glu	tgg Trp 790	aca Thr	tct Ser	gtg Val	gtt Val	gtg Val 795	gca Ala	aat Asn	gta Val	2523
tcc Ser 800	aaa Lys	tat Tyr	att Ile	gtc Val	tca Ser	ggc Gly 805	acg Thr	cca Pro	acc Thr	ttt Phe	gtt Val 810	cca Pro	tac Tyr	ctg Leu	atc Ile	2571
aaa Lys 815	gtt Val	cag Gln	gcc Ala	ctg Leu	aat Asn 820	gac Asp	atg Met	ggg Gly	ttt Phe	gcc Ala 825	ccc Pro	gag Glu	cca Pro	gct Ala	gta Val 830	2619
gtc Val	atg Met	gga Gly	cat His	tct Ser 835	gga Gly	gaa Glu	gac Asp	ctc Leu	cca Pro 840	atg Met	gtg Val	gct Ala	cct Pro	ggg Gly 845	aac Asn	2667
gtg Val	cgt Arg	gtg Val	aat Asn 850	gtg Val	gtg Val	aac Asn	agt Ser	acc Thr 855	tta Leu	gcc Ala	gag Glu	gtg Val	cac His 860	tgg Trp	gac Asp	2715
cca Pro	gta Val	cct Pro 865	ctg Leu	aaa Lys	agc Ser	atc Ile	cga Arg 870	gga Gly	cac His	cta Leu	caa Gln	ggc Gly 875	tat Tyr	cgg Arg	att Ile	2763
tac Tyr 880	tat Tyr	tgg Trp	aag Lys	acc Thr	cag Gln	agt Ser 885	tca Ser	tct Ser	aaa Lys	aga Arg	aac Asn 890	aga Arg	cgt Arg	cac His	att Ile	2811
gag Glu 895	aaa Lys	aag Lys	atc Ile	ctc Leu	acc Thr 900	ttc Phe	caa Gln	ggc Gly	agc Ser	aag Lys 905	act Thr	cat His	ggc Gly	atg Met	ttg Leu 910	2859
ccg Pro	ggg Gly	cta Leu	gag Glu	ccc Pro	ttt Phe	agc Ser	cac His	tac Tyr	aca Thr	ctg Leu	aat Asn	gtc Val	cga Arg	gtg Val	gtc Val	2907

20093A-21US-Substitute Sequence Listing.txt
915 920 925

aat ggg aaa ggg gag ggc cca gcc agc cct gac aga gtc ttt aat act	2955
Asn Gly Lys Gly Glu Gly Pro Ala Ser Pro Asp Arg Val Phe Asn Thr	
930 935 940	
cca gaa gga gtc ccc agt gct ccc tcg tct ttg aag att gtg aat cca	3003
Pro Glu Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile Val Asn Pro	
945 950 955	
aca ctg gac tct ctc act ttg gaa tgg gat cca ccg agc cac ccg aat	3051
Thr Leu Asp Ser Leu Thr Leu Glu Trp Asp Pro Pro Ser His Pro Asn	
960 965 970	
ggc att ttg aca gag tac acc tta aag tat cag cca att aac agc aca	3099
Gly Ile Leu Thr Glu Tyr Thr Leu Lys Tyr Gln Pro Ile Asn Ser Thr	
975 980 985 990	
cat gaa tta ggc cct ctg gta gat ttg aaa att cct gcc aac aag aca	3147
His Glu Leu Gly Pro Leu Val Asp Leu Lys Ile Pro Ala Asn Lys Thr	
995 1000 1005	
cgg tgg act tta aaa aat tta aat ttc agc act cga tat aag ttt tat	3195
Arg Trp Thr Leu Lys Asn Leu Asn Phe Ser Thr Arg Tyr Lys Phe Tyr	
1010 1015 1020	
ttc tat gca caa aca tca gca gga tca gga agt caa att aca gag gaa	3243
Phe Tyr Ala Gln Thr Ser Ala Gly Ser Gly Ser Gln Ile Thr Glu Glu	
1025 1030 1035	
gca gta aca act gtg gat gaa gct ggt att ctt cca cct gat gta ggt	3291
Ala Val Thr Thr Val Asp Glu Ala Gly Ile Leu Pro Pro Asp Val Gly	
1040 1045 1050	
gca ggc aaa gtt caa gct gta aat acc agg atc agc aat ctt act gct	3339
Ala Gly Lys Val Gln Ala Val Asn Thr Arg Ile Ser Asn Leu Thr Ala	
1055 1060 1065 1070	
gca gct gct gag acc tat gcc aat atc agt tgg gaa tat gag gga cca	3387
Ala Ala Ala Glu Thr Tyr Ala Asn Ile Ser Trp Glu Tyr Glu Gly Pro	
1075 1080 1085	
gag cat gtg aac ttt tat gtt gaa tat ggt gta gca ggc agc aaa gaa	3435
Glu His Val Asn Phe Tyr Val Glu Tyr Gly Val Ala Gly Ser Lys Glu	
1090 1095 1100	
gaa tgg aga aaa gaa att gta aat ggt tct cgg agc ttc ttt ggg tta	3483
Glu Trp Arg Lys Glu Ile Val Asn Gly Ser Arg Ser Phe Phe Gly Leu	
1105 1110 1115	
aag ggt cta atg cca gga aca gca tac aaa gtt cga gtt ggt gct gtg	3531
Lys Gly Leu Met Pro Gly Thr Ala Tyr Lys Val Arg Val Gly Ala Val	
1120 1125 1130	
ggg gac tct ggt ttt gtg agt tca gag gat gtg ttt gag aca ggc cca	3579
Gly Asp Ser Gly Phe Val Ser Ser Glu Asp Val Phe Glu Thr Gly Pro	
1135 1140 1145 1150	
gcg atg gca agc cgg cag gtg gat att gca act cag ggc tgg ttc att	3627
Ala Met Ala Ser Arg Gln Val Asp Ile Ala Thr Gln Gly Trp Phe Ile	
1155 1160 1165	
ggt ctg atg tgt gct gtt gct ctc ctt atc tta att ttg ctg att gtt	3675
Gly Leu Met Cys Ala Val Ala Leu Leu Ile Leu Ile Leu Leu Ile Val	
1170 1175 1180	
tgc ttc atc aga aga aac aag ggt ggt aaa tat cca gtt aaa gaa aag	3723

20093A-21US-Substitute Sequence Listing.txt

Cys Phe Ile Arg Arg Asn Lys Gly Gly Lys Tyr Pro Val Lys Glu Lys
1185 1190 1195

gaa gat gcc cat gct gac cct gaa atc cag cct atg aag gaa gat gat 3771
Glu Asp Ala His Ala Asp Pro Glu Ile Gln Pro Met Lys Glu Asp Asp
1200 1205 1210

ggg aca ttt gga gaa tac agt gat gca gaa gac cac aag cct ttg aaa 3819
Gly Thr Phe Gly Glu Tyr Ser Asp Ala Glu Asp His Lys Pro Leu Lys
1215 1220 1225 1230

aaa gga agt cga act cct tca gac agg act gtg aaa aaa gaa gat agt 3867
Lys Gly Ser Arg Thr Pro Ser Asp Arg Thr Val Lys Lys Glu Asp Ser
1235 1240 1245

gac gac agc cta gtt gac tat gga gaa ggg gtt aat ggc cag ttc aat 3915
Asp Asp Ser Leu Val Asp Tyr Gly Glu Gly Val Asn Gly Gln Phe Asn
1250 1255 1260

gag gat ggc tcc ttt att gga caa tac agt ggt aag aaa gag aaa gag 3963
Glu Asp Gly Ser Phe Ile Gly Gln Tyr Ser Gly Lys Lys Glu Lys Glu
1265 1270 1275

ccg gct gaa gga aac gaa agc tca gag gca cct tct cct gtc aac gcc 4011
Pro Ala Glu Gly Asn Glu Ser Ser Glu Ala Pro Ser Pro Val Asn Ala
1280 1285 1290

atg aat tcc ttt gtt taa tttttaagct caaagccaat attccatttc 4059
Met Asn Ser Phe Val
1295 1300

tctagaatgt ttatcctaag ctcttgtttg tcagccctct catactatga acatatgggt 4119

agagagtata ttttc 4134

<210> 2
<211> 1299
<212> PRT
<213> Homo sapiens

<400> 2
Met Pro Lys Lys Lys Arg Leu Ser Ala Gly Arg Val Pro Leu Ile Leu
1 5 10 15
Phe Leu Cys Gln Met Ile Ser Ala Leu Glu Val Pro Leu Asp Pro Lys
20 25 30
Leu Leu Glu Asp Leu Val Gln Pro Pro Thr Ile Thr Gln Gln Ser Pro
35 40 45
Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile Val Ile Gln Cys Glu
50 55 60
Ala Lys Gly Lys Pro Pro Pro Ser Phe Ser Trp Thr Arg Asn Gly Thr
65 70 75 80
His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr Met Lys Pro Gly Thr
85 90 95
Gly Thr Leu Ile Ile Asn Ile Met Ser Glu Gly Lys Ala Glu Thr Tyr
100 105 110
Glu Gly Val Tyr Gln Cys Thr Ala Arg Asn Glu Arg Gly Ala Ala Val
115 120 125
Ser Asn Asn Ile Val Val Arg Pro Ser Arg Ser Pro Leu Trp Thr Lys

20093A-21US-Substitute Sequence Listing.txt

130	135	140													
Glu 145	Lys	Leu	Glu	Pro	Ile 150	Thr	Leu	Gln	Ser	Gly 155	Gln	Ser	Leu	Val	Leu 160
Pro	Cys	Arg	Pro	Pro 165	Ile	Gly	Leu	Pro	Pro 170	Pro	Ile	Ile	Phe	Trp 175	Met
Asp	Asn	Ser	Phe 180	Gln	Arg	Leu	Pro	Gln 185	Ser	Glu	Arg	Val	Ser 190	Gln	Gly
Leu	Asn	Gly 195	Asp	Leu	Tyr	Phe	Ser 200	Asn	Val	Leu	Pro	Glu 205	Asp	Thr	Arg
Glu 210	Asp	Tyr	Ile	Cys	Tyr	Ala 215	Arg	Phe	Asn	His	Thr 220	Gln	Thr	Ile	Gln
Gln 225	Lys	Gln	Pro	Ile	Ser 230	Val	Lys	Val	Ile	Ser 235	Val	Asp	Glu	Leu	Asn 240
Asp	Thr	Ile	Ala	Ala 245	Asn	Leu	Ser	Asp	Thr 250	Glu	Phe	Tyr	Gly	Ala 255	Lys
Ser	Ser	Arg	Glu 260	Arg	Pro	Pro	Thr	Phe 265	Leu	Thr	Pro	Glu	Gly 270	Asn	Ala
Ser	Asn	Lys 275	Glu	Glu	Leu	Arg	Gly 280	Asn	Val	Leu	Ser	Leu 285	Glu	Cys	Ile
Ala 290	Glu	Gly	Leu	Pro	Thr	Pro 295	Ile	Ile	Tyr	Trp	Ala 300	Lys	Glu	Asp	Gly
Met 305	Leu	Pro	Lys	Asn	Arg 310	Thr	Val	Tyr	Lys	Asn 315	Phe	Glu	Lys	Thr	Leu 320
Gln	Ile	Ile	His	Val 325	Ser	Glu	Ala	Asp	Ser 330	Gly	Asn	Tyr	Gln	Cys 335	Ile
Ala	Lys	Asn	Ala 340	Leu	Gly	Ala	Ile	His 345	His	Thr	Ile	Ser	Val 350	Arg	Val
Lys	Ala	Ala 355	Pro	Tyr	Trp	Ile	Thr 360	Ala	Pro	Gln	Asn	Leu 365	Val	Leu	Ser
Pro	Gly 370	Glu	Asp	Gly	Thr	Leu 375	Ile	Cys	Arg	Ala	Asn 380	Gly	Asn	Pro	Lys
Pro 385	Arg	Ile	Ser	Trp	Leu 390	Thr	Asn	Gly	Val	Pro 395	Ile	Glu	Ile	Ala	Pro 400
Asp	Asp	Pro	Ser	Arg 405	Lys	Ile	Asp	Gly	Asp 410	Thr	Ile	Ile	Phe	Ser 415	Asn
Val	Gln	Glu	Arg 420	Ser	Ser	Ala	Val	Tyr 425	Gln	Cys	Asn	Ala	Ser 430	Asn	Glu
Tyr	Gly	Tyr 435	Leu	Leu	Ala	Asn 440	Phe	Val	Asn	Val	Leu 445	Ala	Glu	Pro	
Pro	Arg 450	Ile	Leu	Thr	Pro	Ala 455	Asn	Thr	Leu	Tyr	Gln 460	Val	Ile	Ala	Asn
Arg 465	Pro	Ala	Leu	Leu	Asp 470	Cys	Ala	Phe	Phe	Gly 475	Ser	Pro	Leu	Pro	Thr 480
Ile	Glu	Trp	Phe	Lys 485	Gly	Ala	Lys	Gly	Ser 490	Ala	Leu	His	Glu	Asp 495	Ile

20093A-21US-Substitute Sequence Listing.txt

Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile Lys Asp Ala Thr Trp
 500 505 510
 Ile Val Lys Glu Ile Pro Val Ala Gln Lys Asp Ser Thr Gly Thr Tyr
 515 520 525
 Thr Cys Val Ala Arg Asn Lys Leu Gly Met Ala Lys Asn Glu Val His
 530 535 540
 Leu Gln Pro Glu Tyr Ala Val Val Gln Arg Gly Ser Met Val Ser Phe
 545 550 555 560
 Glu Cys Lys Val Lys His Asp His Thr Leu Ser Leu Thr Val Leu Trp
 565 570 575
 Leu Lys Asp Asn Arg Glu Leu Pro Ser Asp Glu Arg Phe Thr Val Asp
 580 585 590
 Lys Asp His Leu Val Val Ala Asp Val Ser Asp Asp Asp Ser Gly Thr
 595 600 605
 Tyr Thr Cys Val Ala Asn Thr Thr Leu Asp Ser Val Ser Ala Ser Ala
 610 615 620
 Val Leu Ser Val Val Ala Pro Thr Pro Thr Pro Ala Pro Val Tyr Asp
 625 630 635 640
 Val Pro Asn Pro Pro Phe Asp Leu Glu Leu Thr Asp Gln Leu Asp Lys
 645 650 655
 Ser Val Gln Leu Ser Trp Thr Pro Gly Asp Asp Asn Asn Ser Pro Ile
 660 665 670
 Thr Lys Phe Ile Ile Glu Tyr Glu Asp Ala Met His Lys Pro Gly Leu
 675 680 685
 Trp His His Gln Thr Glu Val Ser Gly Thr Gln Thr Thr Ala Gln Leu
 690 695 700
 Lys Leu Ser Pro Tyr Val Asn Tyr Ser Phe Arg Val Met Ala Val Asn
 705 710 715 720
 Ser Ile Gly Lys Ser Leu Pro Ser Glu Ala Ser Glu Gln Tyr Leu Thr
 725 730 735
 Lys Ala Ser Glu Pro Asp Lys Asn Pro Thr Ala Val Glu Gly Leu Gly
 740 745 750
 Ser Glu Pro Asp Asn Leu Glu Ile Thr Trp Lys Pro Leu Asn Gly Phe
 755 760 765
 Glu Ser Asn Gly Pro Gly Leu Gln Tyr Lys Val Ser Trp Arg Gln Lys
 770 775 780
 Asp Gly Asp Asp Glu Trp Thr Ser Val Val Val Ala Asn Val Ser Lys
 785 790 795 800
 Tyr Ile Val Ser Gly Thr Pro Thr Phe Val Pro Tyr Leu Ile Lys Val
 805 810 815
 Gln Ala Leu Asn Asp Met Gly Phe Ala Pro Glu Pro Ala Val Val Met
 820 825 830
 Gly His Ser Gly Glu Asp Leu Pro Met Val Ala Pro Gly Asn Val Arg
 835 840 845

20093A-21US-Substitute Sequence Listing.txt

Val Asn Val Val Asn Ser Thr Leu Ala Glu Val His Trp Asp Pro Val
850 855 860

Pro Leu Lys Ser Ile Arg Gly His Leu Gln Gly Tyr Arg Ile Tyr Tyr
865 870 875 880

Trp Lys Thr Gln Ser Ser Ser Lys Arg Asn Arg Arg His Ile Glu Lys
885 890 895

Lys Ile Leu Thr Phe Gln Gly Ser Lys Thr His Gly Met Leu Pro Gly
900 905 910

Leu Glu Pro Phe Ser His Tyr Thr Leu Asn Val Arg Val Val Asn Gly
915 920 925

Lys Gly Glu Gly Pro Ala Ser Pro Asp Arg Val Phe Asn Thr Pro Glu
930 935 940

Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile Val Asn Pro Thr Leu
945 950 955 960

Asp Ser Leu Thr Leu Glu Trp Asp Pro Pro Ser His Pro Asn Gly Ile
965 970 975

Leu Thr Glu Tyr Thr Leu Lys Tyr Gln Pro Ile Asn Ser Thr His Glu
980 985 990

Leu Gly Pro Leu Val Asp Leu Lys Ile Pro Ala Asn Lys Thr Arg Trp
995 1000 1005

Thr Leu Lys Asn Leu Asn Phe Ser Thr Arg Tyr Lys Phe Tyr Phe Tyr
1010 1015 1020

Ala Gln Thr Ser Ala Gly Ser Gly Ser Gln Ile Thr Glu Glu Ala Val
1025 1030 1035 1040

Thr Thr Val Asp Glu Ala Gly Ile Leu Pro Pro Asp Val Gly Ala Gly
1045 1050 1055

Lys Val Gln Ala Val Asn Thr Arg Ile Ser Asn Leu Thr Ala Ala Ala
1060 1065 1070

Ala Glu Thr Tyr Ala Asn Ile Ser Trp Glu Tyr Glu Gly Pro Glu His
1075 1080 1085

Val Asn Phe Tyr Val Glu Tyr Gly Val Ala Gly Ser Lys Glu Glu Trp
1090 1095 1100

Arg Lys Glu Ile Val Asn Gly Ser Arg Ser Phe Phe Gly Leu Lys Gly
1105 1110 1115 1120

Leu Met Pro Gly Thr Ala Tyr Lys Val Arg Val Gly Ala Val Gly Asp
1125 1130 1135

Ser Gly Phe Val Ser Ser Glu Asp Val Phe Glu Thr Gly Pro Ala Met
1140 1145 1150

Ala Ser Arg Gln Val Asp Ile Ala Thr Gln Gly Trp Phe Ile Gly Leu
1155 1160 1165

Met Cys Ala Val Ala Leu Leu Ile Leu Ile Leu Leu Ile Val Cys Phe
1170 1175 1180

Ile Arg Arg Asn Lys Gly Gly Lys Tyr Pro Val Lys Glu Lys Glu Asp
1185 1190 1195 1200

Ala His Ala Asp Pro Glu Ile Gln Pro Met Lys Glu Asp Asp Gly Thr

20093A-21US-Substitute Sequence Listing.txt
1205 1210 1215

Phe Gly Glu Tyr Ser Asp Ala Glu Asp His Lys Pro Leu Lys Lys Gly
1220 1225 1230
Ser Arg Thr Pro Ser Asp Arg Thr Val Lys Lys Glu Asp Ser Asp Asp
1235 1240 1245
Ser Leu Val Asp Tyr Gly Glu Gly Val Asn Gly Gln Phe Asn Glu Asp
1250 1255 1260
Gly Ser Phe Ile Gly Gln Tyr Ser Gly Lys Lys Glu Lys Glu Pro Ala
1265 1270 1275 1280
Glu Gly Asn Glu Ser Ser Glu Ala Pro Ser Pro Val Asn Ala Met Asn
1285 1290 1295
Ser Phe Val

<210> 3
<211> 38
<212> DNA
<213> Homo sapiens

<400> 3
tctcatacta tgaacatatg ggtagagagt atatttttc 38

<210> 4
<211> 123
<212> DNA
<213> Rattus norvegicus

<400> 4
tctcatacta tggacatatg ggtagaaaga atgttttctg cggtatatga gtattataag 60
aacagagcaa gaacataact cagtcagtca gatgatacgt taatatgaac tgggggtgaaa 120
agg 123

<210> 5
<211> 176
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: clone D4-1

<400> 5
tctcatacta tgaacatatg ggtagagagt atatttttctg ctgtatgtta gtattatgag 60
aatagttaca gcaaaaacat aactcagtca aagtatatgt taatatgaac tgggaatgcaa 120
aagtgcatac tttttcattc aaaatgggta ttcttgattt cctaaaaaaaa aaaaaa 176

<210> 6
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 6

20093A-21US-Substitute Sequence Listing.txt 38

tagatacaac tagtcaatgc ctctaatagaa tatggata

<210> 7
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 7
 agatagatcc gcggaatagt aaatccgata gccttgta 38

<210> 8
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <221> CDS
 <222> (1)
 <223> n=a, c, g, or t

<400> 8
 ngctgctctc atact 15

<210> 9
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 9
 aacatatggg tagagagtat attt 24

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 10
 ctttgcatc cagttcatat taa 23

<210> 11
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 11
 tgtggtgaca gatcacggct 20

20093A-210S-Substitute Sequence Listing.txt

<210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 12
 cagctcaaac ctgtgatttc c 21

<210> 13
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 13
 aataggtatt ggtgaattta aagactcact ctccataaat gctacgaata ttaaactt 60

<210> 14
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 14
 cggagcaata tgaaatgatc t 21

<210> 15
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 15
 gcaaatacag ctcctattg 19

<210> 16
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 16
 gctgtatggt agtattatga gaatagttac agcaaaaaca taa 43

<210> 17
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>

20093A-21US-Substitute Sequence Listing.txt

<223> Description of Artificial Sequence: primer

<400> 17
taggcctgac tggcattgta ttagcaaact catcactaga 40

<210> 18
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18
tagatacaac tagtctaatag cagcttaaaa taatgcc 37

<210> 19
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 19
agatagatcc gcggatatcc atattcatta gaggcattg 39

<210> 20
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 20
tagatacaac tagtcaatgc ctctaataa tatggata 38

<210> 21
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 21
agatagatcc gcggaatagt aaatccgata gccttgta 38

<210> 22
<211> 61
<212> DNA
<213> Homo sapiens

<220>
<223> Description of Artificial Sequence: primer

<400> 22
aggagttaag atgctaatagc agcttaaaat aatgccgaaa aagaagcgct tatctgcggg 60
c 61

20093A-21US-Substitute Sequence Listing.txt

<210> 23
 <211> 19
 <212> DNA
 <213> Homo sapiens

 <400> 23
 cattagcatc ttaactcct 19

 <210> 24
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 24
 tcggcattat ttttaagctgc a 21

 <210> 25
 <211> 17
 <212> DNA
 <213> Homo sapiens

 <400> 25
 gcagataagc gcttctt 17

 <210> 26
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 26
 actagagata cagatcatat 20

 <210> 27
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 27
 catatacgat cgatcgatgc 20

 <210> 28
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 28
 gatagtgctg atcgatgcta 20

 <210> 29
 <211> 48
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 29
 catacgaatt ctagatacaa ctagtctaata gcagcttaaa ataatgcc 48

20093A-21US-Substitute Sequence Listing.txt

<210> 30
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 30
 agatagatcc gcggatatcc atattcatta gaggcattgg gatcccatcac 50

<210> 31
 <211> 1371
 <212> DNA
 <213> Homo sapiens

<400> 31
 atgccgaaaa agaagcgctt atctgcgggc agagtgtccc tgattctctt cctgtgccag 60
 atgattagtg cactggaagt acctcttgat ccaaaacttc ttgaagactt ggtacagcct 120
 ccaaccatca cccaacagtc tccaaaagat tacattattg accctcggga gaatattgta 180
 atccagtgtg aagccaaagg gaaaccgccc ccaagctttt cctggaccgc taatgggact 240
 cattttgaca tcgataaaga ccctctggtc accatgaagc ctggcacagg aacgctcata 300
 attaacatca tgagcgaagg gaaagctgag acctatgaag gagtctatca gtgtacagca 360
 aggaacgaac gcggagctgc agtttctaata aacattgttg tccgcccata cagatcacca 420
 ttgtggacca aagaaaaact tgaaccaatc acacttcaaa gtggtcagtc tttagtactt 480
 ccctgcagac cccaatttg attaccacca cctataatat tttggatgga taattccttt 540
 caaagacttc cacaaagtga gagagtttct caaggtttga atggggacct ttatttttcc 600
 aatgtcctcc cagaggacac ccgcgaagac tatatctgtt atgctagatt taatcatact 660
 caaaccatac agcagaagca acctatttct gtgaagggtga tttcagtgga tgaattgaat 720
 gacactatag ctgctaattt gagtgacact gagttttatg gtgctaaatc aagtagagag 780
 aggccaccaa catttttaac tccagaaggc aatgcaagta acaaagagga attaagagga 840
 aatgtgcttt cactggagtg cattgcagaa ggactgccta cccaattat ttactgggca 900
 aaggaagatg gaatgctacc caaaaacagg acagtttata agaactttga gaaaaccttg 960
 cagatcattc atgtttcaga agcagactct ggaaattacc aatgtatagc aaaaaatgca 1020
 ttaggagcca tccaccatac catttctgtt agagttaaag cggctccata ctggatcaca 1080
 gccctcaaaa atcttgtgct gtccccagga gaggatggga ccttgatctg cagagctaata 1140
 ggcaacccca aaccagaat tagctgggta acaaaggag tccaataga aattgcccct 1200
 gatgacccca gcagaaaaat agatggcgat accattattt tttcaaatgt tcaagaaaga 1260
 tcaagtgcag tatatcagtg caatgcctct aatgaatatg gatatttact ggcaaacgca 1320
 tttgtaaatg tgctggctga gccaccacga atcctcacac ctgcaaacac a 1371

<210> 32
 <211> 1371

20093A-21US-Substitute Sequence Listing.txt

<212> DNA

<213> Rattus norvegicus

<400> 32

```

atgccgaaga agaagccctt gtctgcaggc agagcgcccc tgtttctctt cctgtgccag 60
atgatcagcg ctctggatgt tcctcttgat ccaaagctcc ttgatgactt ggtacagcct 120
ccaactatca ctcaacagtc accaaaagac tacatcattg acccacggga gaatattgta 180
atccaatgtg aggccaaagg gaaacctcct ccaagctttt cctggactcg taacggaaca 240
cattttgaca tagacaaaga ccctctggtc actatgaagc ctggctcagg aacccttgtc 300
atcaacatca tgagtgaagg aaaggcggag acctatgaag gggtttacca gtgcactgca 360
aggaatgagc gcggagctgc tgtctccaat aacattgttg tccgcccctc taggtcaccc 420
ttgtggacca aggaaagact tgaaccaata atcctccgaa gtggtcagtc actagtacta 480
ccatgtaggc ctccaattgg attaccaccg gccataatat ttggatgga taactccttt 540
caaagactgc cacagagtga gcgggtttcc caaggactga atggagacct ttacttctcc 600
aatgtcctcc cagaggacac ccgtgaggac tacatctgct atgccagatt taatcacact 660
caaacaattc aacagaaaca acctatttct ctgaagggtga ttccagtgga tgaattgaat 720
gacactatag ctgctaattt gagtgcactt gagttttatg gtgctaaatc tagtaaagag 780
aggccaccaa catttctaac tccagagggc aatgaaagtc acaaggaaga attaagagga 840
aacgtgcttt ccctggagtg cattgcagaa ggcctaccta ctccagttat ttactggatc 900
aaggaagatg gaacgcttcc tgtcaaccgg acgttttatc ggaactttaa gaaaaccttg 960
cagatcattc atgtctctga agcagactct ggaaattatc agtgcatagc aaaaaacgca 1020
ttgggagccg tccatcatac catttctgtc acagttaaag cggctcccta ctggattgtt 1080
gcacctcaca acctcgtgct ttccccaggg gagaatggga ccctcatctg cagagctaac 1140
ggcaacccaa aaccagaat tagctgggta acaaatggag tcccagtaga aattgctctc 1200
gatgacccca gccgaaaaat cgatgggtgat accattatgt tttcaaatgt tcaagaaagc 1260
tcaagtgcgg tttatcagtg caatgcctct aacaaatatg gatatttact agcaaatgca 1320
tttgtaaatt tgctcgtga accacctcgg attcttacct cagcaaacac a 1371

```

<210> 33

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pLXSN MCS (EcoRI and BamHI cloning site)

<400> 33

gcgccggaat tcgttaacct cgaggatccg gctgtg

36